

3/01



#2

OIEPE

RAW SEQUENCE LISTING

DATE: 02/27/2002

PATENT APPLICATION: US/10/067,482

TIME: 08:26:01

Input Set : A:\1U 102 R1.ST25.txt

Output Set: N:\CRF3\02272002\J067482.raw

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3 <110> APPLICANT: OriGene Technologies, Inc.
 5 <120> TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
 7 <130> FILE REFERENCE: 1U 102 R1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/067,482
 C--> 9 <141> CURRENT FILING DATE: 2002-02-07
 9 <160> NUMBER OF SEQ ID NOS: 4
 11 <170> SOFTWARE: PatentIn version 3.1
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 14 <211> LENGTH: 3727
 15 <212> TYPE: DNA
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 29 gac ttg gtg tgg ggg aaa ctc ggc cga tat cct cct tgg cca gga aag 102
 30 Asp Leu Val Trp Gly Lys Leu Gly Arg Tyr Pro Pro Trp Pro Gly Lys
 31 10 15 20 25
 33 att gtt aat cca cca aag gac ttg aag aaa cct cgc gga aag aaa tgc 150
 34 Ile Val Asn Pro Pro Lys Asp Leu Lys Lys Pro Arg Gly Lys Lys Cys
 35 30 35 40
 37 ttc ttt gtg aaa ttt ttt gga aca gaa gat cat gcc tgg atc aaa gtg 198
 38 Phe Phe Val Lys Phe Phe Gly Thr Glu Asp His Ala Trp Ile Lys Val
 39 45 50 55
 41 gaa cag ctg aag cca tat cat gct cat aaa gag gaa atg ata aaa att 246
 42 Glu Gln Leu Lys Pro Tyr His Ala His Lys Glu Glu Met Ile Lys Ile
 43 60 65 70
 45 aac aag ggt aaa cga ttc cag caa gcg gta gat gct gtc gaa gag ttc 294
 46 Asn Lys Gly Lys Arg Phe Gln Gln Ala Val Asp Ala Val Glu Glu Phe
 47 75 80 85
 49 ctc agg aga gcc aaa ggg aaa gac cag acg tca tcc cac aat tct tct 342
 50 Leu Arg Arg Ala Lys Gly Lys Asp Gln Thr Ser Ser His Asn Ser Ser
 51 90 95 100 105
 53 gat gac aag aat cga cgt aat tcc agt gag gag aga agt agg cca aac 390
 54 Asp Asp Lys Asn Arg Arg Asn Ser Ser Glu Glu Arg Ser Arg Pro Asn
 55 110 115 120
 57 tca ggt gat gag aag cgc aaa ctt agc ctg tct gaa ggg aag gtg aag 438
 58 Ser Gly Asp Glu Lys Arg Lys Leu Ser Leu Ser Glu Gly Lys Val Lys
 59 125 130 135

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65	aga ggc tcc aaa tcc cct ctg aaa aga gcc caa gag caa agt ccc cgg	534
66	Arg Gly Ser Lys Ser Pro Leu Lys Arg Ala Gln Glu Gln Ser Pro Arg	
67	155 160 165	
69	aag cgg ggt cgg ccc cca aag gat gag aag gat ctc acc atc ccg gag	582
70	Lys Arg Gly Arg Pro Pro Lys Asp Glu Lys Asp Leu Thr Ile Pro Glu	
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73	tct agt acc gtg aag ggg atg atg gcc gga ccg atg gcc gcg ttt aaa	630
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75	190 195 200	
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78	Trp Gln Pro Thr Ala Ser Glu Pro Val Lys Asp Ala Asp Pro His Phe	
79	205 210 215	
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82	His His Phe Leu Leu Ser Gln Thr Glu Lys Pro Ala Val Cys Tyr Gln	
83	220 225 230	
85	gca atc acg aag aag ttg aaa ata tgt gaa gag gaa act ggc tcc acc	774
86	Ala Ile Thr Lys Lys Leu Lys Ile Cys Glu Glu Glu Thr Gly Ser Thr	
87	235 240 245	
89	tcc atc cag gca gct gac agc aca gcc gtg aat ggc agc atc aca ccc	822
90	Ser Ile Gln Ala Ala Asp Ser Thr Ala Val Asn Gly Ser Ile Thr Pro	
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93	aca gac aaa aag ata gga ttt ttg ggc ctt ggt ctc atg gga agt gga	870
94	Thr Asp Lys Lys Ile Gly Phe Leu Gly Leu Gly Leu Met Gly Ser Gly	
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97	atc gtc tcc aac ttg cta aaa atg ggt cac aca gtg act gtc tgg aac	918
98	Ile Val Ser Asn Leu Leu Lys Met Gly His Thr Val Thr Val Trp Asn	
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101	cgc act gca gag aaa tgt gat ttg ttc atc cag gag ggg gcc cgt ctg	966
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106	Gly Arg Thr Pro Ala Glu Val Val Ser Thr Cys Asp Ile Thr Phe Ala	
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109	tgc gtg tgc gat ccc aag gcg gcc aag gac ctg gtg ctg ggc ccc agt	1062
110	Cys Val Ser Asp Pro Lys Ala Ala Lys Asp Leu Val Leu Gly Pro Ser	
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113	ggt gtg ctg caa ggg atc cgc cct ggg aag tgc tac gtg gac atg tca	1110
114	Gly Val Leu Gln Gly Ile Arg Pro Gly Lys Cys Tyr Val Asp Met Ser	
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118	Thr Val Asp Ala Asp Thr Val Thr Glu Leu Ala Gln Val Ile Val Ser	
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121	agg ggg ggg cgc ttt ctg gaa gcc ccc gtc tca ggg aat cag cag ctg	1206
122	Arg Gly Gly Arg Phe Leu Glu Ala Pro Val Ser Gly Asn Gln Gln Leu	
123	380 385 390	
125	tct aat gac ggg atg ttg gtg atc tta gcg gct gga gac agg ggc tta	1254

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127		395					400					405					
129	tat	gag	gac	tgc	agc	agc	tgc	ttc	cag	gcg	atg	ggg	aag	acc	tcc	ttc	1302
130	Tyr	Glu	Asp	Cys	Ser	Ser	Cys	Phe	Gln	Ala	Met	Gly	Lys	Thr	Ser	Phe	
131	410					415					420					425	
133	ttc	cta	ggt	gaa	gtg	ggc	aat	gca	gcc	aag	atg	atg	ctg	atc	gtg	aac	1350
134	Phe	Leu	Gly	Glu	Val	Gly	Asn	Ala	Ala	Lys	Met	Met	Leu	Ile	Val	Asn	
135					430					435					440		
137	atg	gtc	caa	ggg	agc	ttc	atg	gcc	act	att	gcc	gag	ggg	ctg	acc	ctg	1398
138	Met	Val	Gln	Gly	Ser	Phe	Met	Ala	Thr	Ile	Ala	Glu	Gly	Leu	Thr	Leu	
139			445						450					455			
141	gcc	cac	gtg	aca	ggc	cag	tcc	cag	cag	aca	ctc	ttg	gac	atc	ctc	aat	1446
142	Ala	His	Val	Thr	Gly	Gln	Ser	Gln	Gln	Thr	Leu	Leu	Asp	Ile	Leu	Asn	
143			460					465						470			
145	cag	gga	cag	ttg	gcc	agc	atc	ttc	ctg	gac	cag	aag	tgc	caa	aat	atc	1494
146	Gln	Gly	Gln	Leu	Ala	Ser	Ile	Phe	Leu	Asp	Gln	Lys	Cys	Gln	Asn	Ile	
147		475					480				485						
149	ctg	caa	gga	aac	ttt	aag	cct	gat	ttc	tac	ctg	aaa	tac	att	cag	aag	1542
150	Leu	Gln	Gly	Asn	Phe	Lys	Pro	Asp	Phe	Tyr	Leu	Lys	Tyr	Ile	Gln	Lys	
151	490				495						500					505	
153	gat	ctc	cgc	tta	gcc	att	gcg	ctg	ggt	gat	gcg	gtc	aac	cat	ccg	act	1590
154	Asp	Leu	Arg	Leu	Ala	Ile	Ala	Leu	Gly	Asp	Ala	Val	Asn	His	Pro	Thr	
155				510					515						520		
157	ccc	atg	gca	gct	gca	gca	aat	gag	gtg	tac	aaa	aga	gcc	aag	gcg	ctg	1638
158	Pro	Met	Ala	Ala	Ala	Ala	Asn	Glu	Val	Tyr	Lys	Arg	Ala	Lys	Ala	Leu	
159			525						530					535			
161	gac	cag	tcc	gac	aac	gat	atg	tcc	gcc	gtg	tac	cga	gcc	tac	ata	cac	1686
162	Asp	Gln	Ser	Asp	Asn	Asp	Met	Ser	Ala	Val	Tyr	Arg	Ala	Tyr	Ile	His	
163		540					545				550						
165	taa	gctgtcgaca	ccccgccctc	acccctccaa	tccccctct	gacccccctct											1739
167	tcctcacatg	gggtcggggg	cctgggagtt	cattctggac	cagcccacct	atctccattt											1799
169	ccttttatac	agactttgag	acttgccatc	agcacagcac	acagcagcac	ccttccccctg											1859
171	aggccggtgg	ggaggggaca	agtgtcagca	ggattggcgt	gtgggaaagc	tcttgagctg											1919
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175	ggctctcgcc	ccaggataga	agctgcccag	aaactgctgc	ctggcttttt	ttcttccgag											2039
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185	gtgtgcaccc	agcgtcccat	agacgccttt	gtgaactgaa	aagagactgg	cagagtcccc											2339
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193	ctcagggcca	ctagtgtgta	gccaaagaga	gtgggggttg	ggggcgctcc	tttctgtttc											2579
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197	agtggtccca	ccttctccac	cctgcccctgc	caagtcccct	gcatgcccac	cgctctccat											2699
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201	cccagaccca	gctgaccaa	cgatgagcat	ttcttaggct	cagctcttga	tacggaaacg											2819
203	agtgtcttca	ctccagccag	catcatggct	ttcgggtgct	cccgggcccc	gggtctgtcg											2879

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209 gcaaaaaaaaa aagttaccca agggatgtca gttttttatc cctctgcatg ggttggattt 3059
211 tccaaaatca taatttgcag aaggaaggcc agcatttatg atgcaatatg taattatata 3119
213 taggggtggcc acactagggc ggggtccttc cccctcaca gctttggccc ctttcagaga 3179
215 ttagaaaactg ggtagagga ttgcagaaga cgagtggggg gagggcaggg aagatgcctg 3239
217 tcgggttttt agcacagttc atttcaactg gattttgaag ctttctgtc tgaacacaaa 3299
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221 aaccggttag tcaattttgt cttaatattg ttgacaattc tgtaaagttc ctttttatga 3419
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229 tgtctttcag aataggattg tgtgataatg tttaaatggc aaaaacaaaa catgattttg 3659
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251 Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly
252 35 40 45
255 Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His
256 50 55 60
259 Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln
260 65 70 75 80
263 Gln Ala Val Asp Ala Val Glu Glu Phe Leu Arg Arg Ala Lys Gly Lys
264 85 90 95
267 Asp Gln Thr Ser Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn
268 100 105 110
271 Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys
272 115 120 125
275 Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys
276 130 135 140
279 Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu
280 145 150 155 160
283 Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys
284 165 170 175
287 Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met
288 180 185 190
291 Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu
292 195 200 205
295 Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln
296 210 215 220
299 Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys

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311 Leu Gly Leu Gly Leu Met Gly Ser Gly Ile Val Ser Asn Leu Leu Lys
312          275          280          285
315 Met Gly His Thr Val Thr Val Trp Asn Arg Thr Ala Glu Lys Cys Asp
316          290          295          300
319 Leu Phe Ile Gln Glu Gly Ala Arg Leu Gly Arg Thr Pro Ala Glu Val
320 305          310          315          320
323 Val Ser Thr Cys Asp Ile Thr Phe Ala Cys Val Ser Asp Pro Lys Ala
324          325          330          335
327 Ala Lys Asp Leu Val Leu Gly Pro Ser Gly Val Leu Gln Gly Ile Arg
328          340          345          350
331 Pro Gly Lys Cys Tyr Val Asp Met Ser Thr Val Asp Ala Asp Thr Val
332          355          360          365
335 Thr Glu Leu Ala Gln Val Ile Val Ser Arg Gly Gly Arg Phe Leu Glu
336          370          375          380
339 Ala Pro Val Ser Gly Asn Gln Gln Leu Ser Asn Asp Gly Met Leu Val
340 385          390          395          400
343 Ile Leu Ala Ala Gly Asp Arg Gly Leu Tyr Glu Asp Cys Ser Ser Cys
344          405          410          415
347 Phe Gln Ala Met Gly Lys Thr Ser Phe Phe Leu Gly Glu Val Gly Asn
348          420          425          430
351 Ala Ala Lys Met Met Leu Ile Val Asn Met Val Gln Gly Ser Phe Met
352          435          440          445
355 Ala Thr Ile Ala Glu Gly Leu Thr Leu Ala His Val Thr Gly Gln Ser
356          450          455          460
359 Gln Gln Thr Leu Leu Asp Ile Leu Asn Gln Gly Gln Leu Ala Ser Ile
360 465          470          475          480
363 Phe Leu Asp Gln Lys Cys Gln Asn Ile Leu Gln Gly Asn Phe Lys Pro
364          485          490          495
367 Asp Phe Tyr Leu Lys Tyr Ile Gln Lys Asp Leu Arg Leu Ala Ile Ala
368          500          505          510
371 Leu Gly Asp Ala Val Asn His Pro Thr Pro Met Ala Ala Ala Ala Asn
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/067,482

DATE: 02/27/2002

TIME: 08:26:02

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date